



Structure Nucleotide **PMC** OMIM PubMed Protein Genome (Go Clear  $\nabla$ 

Search Protein for

Limits Preview/Index Clipboard History

Details Display\_ default Show: 20 Sendito File  $\overline{\mathbf{v}}$ Get Subsequence

☐ 1: AAA28373. Antennepedia prot...[gi:156934]

BLink, Domains, Links

Books

Taxonomy

AAA28373 LOCUS 74 aa linear INV 26-APR-1993

DEFINITION Antennepedia protein.

AAA28373 ACCESSION

VERSION AAA28373.1 GI:156934

locus DROANTC2 accession K01948.1 **DBSOURCE** 

**KEYWORDS** 

Drosophila melanogaster (fruit fly) SOURCE

Drosophila melanogaster ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (residues 1 to 74) REFERENCE

McGinnis, W., Garber, R.L., Wirz, J., Kuroiwa, A. and Gehring, W.J. AUTHORS

TITLE A homologous protein-coding sequence in Drosophila homeotic genes

and its conservation in other metazoans

**JOURNAL** Cell 37 (2), 403-408 (1984)

MEDLINE 84205674 PUBMED 6327065

COMMENT Method: conceptual translation.

**FEATURES** Location/Qualifiers

1..74 source

/organism="Drosophila melanogaster"

/db xref="taxon:7227" /map="right arm of ch. 3"

Protein 1..74

/name="Antennepedia protein"

CDS

/coded by="complement(K01948.1:<1..>222)"

ORIGIN

11

1 iylepterkr grqtytryqt lelekefhfn ryltrrrrie iahalclter qikiwfqnrr

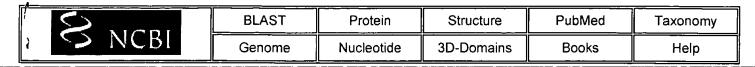
61 mkwkkenktk gepd

Disclaimer | Write to the Help Desk NCBI | NLM | NIH

Apr 24 2003 13:08:07

Score = 61.7 bits (138), Expect = 1e-09 Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 RQIKIWFQNRRMKWKK 16 RQIKIWFQNRRMKWKK Sbjct: 50 RQIKIWFQNRRMKWKK 65



## Query: gi|156934 Antennepedia protein

Best hits Common Tree Texonomy Report 3D structures CDD-Search Clist
200 BLAST hits to 59 unique species Sort by taxonomy proximity
Archaea Bacteria Metazoa Fungi Plants Viruses Other Eukaryotae
Keep only Cut-Off 100 Select Reset

/4 aa					
սուրադասիասիասիասիասի	SCORE	<u>P</u>	ACCESSION	<u>GI</u>	PROTEIN DESCRIPTION
	<u>362</u>	20	AAC31945	3420836	Antennapedia homeotic protein [Anop
	<u> 362</u>	19	BAA04087	<u>391615</u>	Antennapedia homologue protein [Bom
	<u> 362</u>	35	<u> A25399</u>	84890	homeotic protein Antennapedia - fru
	<u>362</u>	34	AA000997	27374237	Antp-PA [Drosophila erecta]
	<u> 362</u>	20	EAA07256	21295111	agCP12956 [Anopheles gambiae str. P
	<u> 362</u>	19	<u> S58850</u>	<u>1363994</u>	homeotic protein abd-A - Junonia co
	<u> 362</u>	32	CAA43307	829192	Antp [Drosophila subobscura]
	<u>357</u>	31	<u>AAA28737</u>	158023	homeobox protein
	<u>357</u>	35	1HOM	<u>443020</u>	Chain , Antennapedia Protein (Home
	<u>355</u>	19	AAF69136	7767519	<pre>prothoraxless [Tribolium castaneum]</pre>
	<u>355</u>	19	<u>AAK96031</u>	15450324	homeodomain transcription factor Pr
	349	19	CAC06383	9967824	Antennapedia protein [Apis mellifer

us-09-654-743-51.rge

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5.1.4_p5_4578
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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(without alignments)
5971.353 Million cell updates/sec
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198
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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em\_htg\_other: em\_htg\_hum:\* em\_htg\_mus:\* em\_htg\_pln:\* em\_htg\_mam:\* em\_or:\* em\_ov:\* em\_pat:\* em\_ro:\* em\_sts: em\_un:  the number of results predicted by chance to have a . 13 No. Pred.

em\_htgo\_mus:\* em\_htgo\_other: em\_htgo\_hum:\*

AX412124 Sequence AR116400 Sequence AR116702 Sequence 088990 Mus musculu U36842 Mus musculu AF1[83429 Rattus no AB033366 Rattus no AF30433 Rattus no AF30433 Rattus no E31042 Method for U32974 Human IAP-1 BC032729 Humo sapi AX429575 Sequence AK101281 Sequence AX412118 Sequence U45880 Human X-1in AX412131 Sequence AK106597 Sequence AK106595 Sequence AK104566 Sequence Homo sapi Sequence Pan trogi Sequence Homo sapi Homo sapi Sequence Sequence Sequence Homo sapi Homo sapi Sequence score greater than or equal to the score of the result  $b_{\perp}^4$ ing printed, and is derived by analysis of the total score distribution. Desdription SUMMARIES AX370789 AX104968 DB % Query Match Length I 79.3 1752 79.3 1752 79.3 1758 75.3 1758 75.3 1758 75.3 144993 75.3 144993 75.3 16401 73.6 711 73.6 711 73.6 711 73.6 711 73.6 711 73.6 711 73.6 711 73.6 711 73.6 711 73.7 1140 73.8 133391 84.3 2011997 38.7 18093 Score 194.8 194.8 194.8 186.8 OO

PAT 15-JUN-2002 Euteleostomi; Murinae; Mus. Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
Antisense lap nucleic acids and uses thereof
Patent: WO 0226968-A 224 04-APR-2002; Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; linear DNA AX412124 Sequence 224 from Patent W0022696B. AX412124 AX412124.1 GI:21444584 house mouse. LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 AX412124

282207 Homo sapien U79142 Sus scrofa AL390123 Human DNA L49432 Homo sapien AR129833 Sequence

ALIGNMENTS

AY030053 Gorilla 9 AP002967 Homo sapi AP003085 Homo sapi

145.

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AF458770 Bos tauru AF451854 Gallus ga AL121601 Human DNA

RESULT 3

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2691 bp mRNA linear Rob 31-MAY-1997 us X-linked inhibitor of apoptosis (miap-3) mRNA, ds.
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   PAT 16-MAY-2001
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... Lefebvre,C., Korneluk,R.G. and MacKenzie,A.E.
mission
(07-FEB-1997) Molecular Genetics, Children's Hospital of
tario, 401 Smyth Rd., Ottawa, Ontario KlH 8Ll, Canada
ocation/Qualifiers
.2691
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1896)
96209843
                                                              2 (bases 1 to 1988)
Vaux, D.L., Uren, A.G. and Pakusch, M.
Direct Submission
Submitted (21-SEP-1995) M. Pakusch, The Walter and
Institute, Royal Parade, Parkville, Victoria 3050,
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Uren, A.G., Pakusch, M., Hawkins, C.J., Puls, K.L. and Vaux, D.L.
Cloning and expression of apoptosis inhibitory protein homologs
that function to inhibit apoptosis and/or bind tumor necrosis
factor receptor-associated factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1461 TATGAAGCACGGATCGTTACTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCTT 1520
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Mus musculus
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Rattus norvegicus clone 2 inhibitor of apoptosis protein 3 mRNA, complete cds.
AF304334.1 GI:11890720
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TOSTSPGIONGQYKSENCVGNRNHFALDRESETHADYLLRYGQVYDISDTIYPRNPAM
TOSTSPGIONGQYKSENCVGNRNHFALDRESETHADYLLRYGQVYDISDTIYPRNPAM
TOSTSPGIONGQYKSENCYGNRNWNSESGYSSDRNFPAMAEYDDARIYTEGTWLY
SYNKEQLARAGEYALGEGDKYKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYTLLDEKG
OEYINNIHLTHSLGESVYRTAEKTPSYTKKIDDTIFQNPWYDEAIRWFNKDIKKTM
ERKLQYSGSNYLSLEVLIADLYSAQKNNSQDESSQYSLQKDISTEGURRLQEEKLCK
ICMDNNIAIVEVPCGHLYTGKOCAAVDKCPWCCTVITFKQKIFMS"
                                                                                                                                Saito.N.
Rattus norvegicus X. linked inhibitor of apoptosis (riap3) mRNA
published Only in DataBase (1999)
2 (bases 1 to 2468)
2 (bases 1 to 2468)
Saito.N.
Direct Submission
Submitted (07-OCT-1999) Nobuhito Saito, University of Tokyo,
Department of Neurosurgery; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655,
Japan (E-mail:nsaito-tky@umin.ac.jp, Tel:+81-3-5800-8853,
Fax:+81-3-5800-6655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BaA85304.1"
/db_xref="G1:6045148"
/translation="MTFNSFEGSRTVVPADTNKDEEFVEEFNRLKTFANFPSSSPVSA
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Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 2.4e-41;
0; Mismatches 10; Indels C
                                             Chordata; Craniata; Vertebrata; E
Rodentia; Sclurognathi; Muridae;
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
Rattus norvegicus cDNA to mRNA.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Rodentia; Ṣ
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/gene="riap3"
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Best Local Similarity 94.9%;
Matches 188; Conservative
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STARAGETTTGEGDTVQCTSCHAAVDNWQVCDSAVGANFRISPNCRTNGFYFENGA
STLARAGETTTGEGDTVQCTSCHAAVDNWQVCDSAVGANFRISPNCRTNGFYFENGA
STERRAPPETSTONGOVERSENCVGRRNHFALDRPSETHADVLLRTGQVVDISDTIYFNDPAM
CSEEARPRTFQNWPDYAHLSPRELASAGLYTTGIDDQVQCFCCGGKLKNWEPCDRAWS
SHRRHPFRCFVLGRNWYRSEGGVSDRNPFRSTUSPRTAAARDTOARIVFFGTWLY
SVNKEQLARAGFYALGSEDKYKCFHCGGGLTDWKPSEDDWSGHAKWPGCKYLLDEKG
OEYINNIHLTHSLGESVVRTAEKTPSVTKKIDDTIFQNPWVGEAIRMGFNFKDIKKTM
ERKLGTGSSNYLSLEVLIADLVSAQKDNSQDESSQTSLQKDISTERGLRRLQEEKLCK
1CMDRNAIAVEVPGGHLVTCKQCCTVITFKQKIFMF"

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    ROD 16-JUL-2002
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  AF183429 1491 bp mRNA linear ROD 16-JUL-200
Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.
Direct Submission
Submitsed (08-582-1999) Department of Biochemistry, Microbiology and Immunology, University of Ottawa, 451 Smyth Road, Ottawa, Ontario KiH 8M5, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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/note="RIAP-3; similar to X-linked IAP (XIAP)"
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Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.

Cloning and characterization of the rat homologues of

of Apoptoals protein 1, 2, and 3 genes

BMC Genomics 3 (1), 5 (2002)
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/protein_id="AAG22969.1"
/db_xref="GI:10765281"
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Rattus norvegicus riap3 mRNA, complete cds.
AB033366.1 GI:6045147
RIAP3.

    1. .1491
    /organism="Rattus norvegicus"

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94.9%;
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Rattus norvegicus
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stlaragelyyggeschaavdrwysterdsgreeningpypering
tostspolowgyrsenvowrnhypladpspethadyllatrogovolsdylyppad
cseearlktpowydyrallsprelasaglyytgiddovygeggekiknwepodraws
ehrrhppncppydrallsprelasaglyytgiddovygeggekiknwepodraws
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Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                    Lareu, R.R., Lacher, M., Frils, R.R. and Dharmarajan, A.M.
Direct Submission
Submitted (OB-SEP-2000) Anatomy and Human Biology, University
Western Australia, Verdum St, Nedlands, WA 6907, Australia
Location, Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
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       1 (bases 1 to 3032)
Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and
Dharmarajan, A.M.
Cloning, characterization and regulation of an inhibitor of
apoptosis protein in the rat corpus luteum
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/db_xref="GI:11890721"
                                                                                                                                                                                                                                                                                                                                          pregnancy"
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/strain="Wistar"
/db_xref="taxon:10116"
/clone="2"
                                                                                                                                                                                                                                                                                                                      /tissue_type="ovary"
/note="isolated at day 15 of
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/note-"IAP3"
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KEYWORDS
SOURCE
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QETINNIHLTHSLGESVVRTAEKTPSVTKTKTDTIFQNPWQBAIRWFPKTLKTK
EGKLGTGGSGSNXLSLEVLIADLVSAQKONSQDSSGTSLGKDISTERGDERKCK
ICWDRAIN AVVFVGGHLVYTCKGCAENVDKCPWCCTVIFFKGKFLCLNFAPQ"
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                                                                                                                                           2 (bases I to 2032)
Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.
Direct Submission
Submitted (08-2500) Anatomy and Human Biology, University of Western Australia, Verdum St, Nedlands, WA 6907, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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                                                       Cloning, characterization and regulation of an inhibitor apoptosis protein in the rat corpus luteum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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S UNIDEDITIES A
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Lareu, R. R., Bradley, C.K., Lacher, M., Frils, R.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="ovary"
/note="isolated at day 15 of pregnancy"
125. 1630
/note="IAP3"

    2032
    /organism="Rattus norvegicus"
    /strain="Wistar"

                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10116"
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E31042.1 GI:13017307
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Kunihiro, M.
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Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369
IMAGE:5532247, mRNA, complete cds.
BC032729.1 GI:21619763
MGC.
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YSEEARLKSEONWPDYAHLTPRELASAGLYYTGIGDQVQCFCCGGKLKNWEPCDRAMS
EHRRHFPNCFFVLGRNINIRSESDAVSSDRNFPNSTNLPRNFSMADYEARIFTFGTWI
                                                                                                                                                                                                                                                                                                                                                               YSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWRPSEDPWEOHAKWYPGCXYLLEOK
GEOTINNIHLTHSLEECLYRTTEKTPSETPSELTREIDDTEONPWOGBAIRWGFSFKDIKKI
MEEK JOSGNYKSLEEZLYADLVNAOKDSMPDESSQYSLOKEISTEEGLRRLQEEKLC
KICMDNIAIVEVPCGGHLVTCKOCABAVDKCPMCYTVITFKOKIFMS"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 2086)

Strausberg, R.

Direct Submission

Sub
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Contact: MGC help desk
Emall: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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Pred. No. 9.4e-39;
0; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= 774
/note= 1AP repeat"
877 . 1068
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                                                                                    /dev_stage="fetus"
32, .1575
                                                                                                                                         /codon_start=1
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Matches 182; Conservative
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SOURCE
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AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 1659)
Duckett, C.S., Nava, V.E., Gedrich, R.W., Clem, R.J., Van Dongen, J.L.,
Gilfillan, M.C., Shiels, H., Hardwick, J.M. and Thompson, C.B.
A conserved family of cellular genes related to the baculovirus tap
gene and encoding apoptosis inhibitors
EMBO J. 15 (11), 2685-2694 (1996)
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                                                                                                                    KUNIHIRO MATSUMOTO
GOIN33/566, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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Direct Submission

Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                      GOIN33/536,GOIN33/536//C12N15/09,C12P21/08,A61K37/02,37/02, PC A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/04,C12N15/00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 173; DB 6; Length 1659;
Préd. No. 9.4e-39;
0; Mismatches 15; Indels
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/db_xref="taxon:9606"
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/organism="unidentified"
/db_xref="taxon:32644"
1 296 c 385 g 459
                                                                  13-MAY-1998 JP 1998130378
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Location/Qualifiers
1. 1659
                  JP 1999326328-A/2
26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                     Topology: Linear;
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illarity 92.4%;
Conservative
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               PN JP 1999
PP 26-NOV-1
PR 13-MAY-1
PR KUNIHIRO
PC GOIN33/5
PC A61K45/0
GOIN33/536,
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PC GOIN33/536,
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PC GOIN37/57/02, PC A6137/00
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           CDNA Library Arrayed by: National Institutes of Health Intramural Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC).

Gaithersburg, Maryland;
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom. Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,
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GQBYINNIHLTHSLEECLVRTTEKTPSELTRRIDDTIFONPWYOEAIRWGFSFKDIKKI
MEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEQLRRLOEEKLC
MEEKIQISGSNYKSLEVLYCKQCABAVDKCPMCYTVIFKQKIFWS"
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STLARAGFLYTGEGDTVRCFSCHAAVDRWQYGDSAVGRHRKVSPNCRFINGFYLENSA
TQSTNSGIQNGQYKVENYLGSRDHFALDRPSETHADYLLRTGQVVDISDTIYPRNPAM
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EHRRHFPDNCFFVLGRNLNIRSESDAVSSDRNFPNSTNLPRNPSMADYBARIFTFGTWI
                                                                                                                                                                                                                                                                                                         be found
                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRRK Plate: 69 Row: j Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502142. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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/protein_id="AaH32729.1"
/db_xref="G1:21619764"
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 Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:45369 IMAGE:5532247"
/tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
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/note="vector: pCMV-SPORT6'
79. .1572
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Sequence 38 from Patent W00226820.
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/db_xref="LocusiD:331"
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Bennett, C.Frank, Ackermann, E.J. and Cowsert, L.M.
Antisense modulation of X-linked inhibitor of apoptosis expression
Patent: US 6087173-A III-JUL-2000;
                                                                            Euteleostom1;
                                                                                                                                Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M., Reinhardt, M.W. and Zusman, S. Transgenic drosophila melanogaster expressing beta amyloid Patent: WO 0226620-A 38 04 APR-2002; NOVARTIS ERFIND VERWALT GMBH (AT) Location/Qualifiers
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Bammalla; Eutheria; Primates; Catarrhini; Hominidae
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Pred. No. 8.8e-39;
0; Mismatches 15; Indels
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92.4%; Pred. No. 8.9e-39;
iive 0; Mismatches 15,
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patent US 6087173.
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/db_xref="taxon:9606"
372 c 525 g 74
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415 c 571 g
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GI:21540833
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92.48;
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                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhinl; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCATT 885
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University of Cutawa (CA); Aegera Therapeutics Inc. (CA) Location/Qualifiers
1. 2540
/organism="Homo sapiens"
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781 a 415 c 570 g 773 t 1 others
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0; Mismatches 15; Indels
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Ax412118
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Best Local Similarity 92.4%;
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Apoptosis inhibitor; x-linked inhibitor of apoptosis protein; M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome; isohaemia; myocardial infarction; stroke; stroke; reperfusion injury; toxin-induced liver disease; gene therapy;
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                               ABK14677
ABK14678
AAD03581
AAA06940
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04-AUG-1995;
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                                                                           April 19, 2003, 00:03:06; Search time 150 Seconds (without alignments) 2972.638 Million cell updates/sec
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         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAPL or HIAP2. Also included are a pharmacentical composition comprising a mammalian IAP antisense molecule and a method of enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for the acid of the action of the cell for the mammal diagnosed with a proliferative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                         treating a patient disposed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer.) adeanocarcinoma, lymphoma, pancreatic cancer.) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a mouse IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGFGGA 120
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                                                                                                                                                         Novel antisense inhibitor of apoptosis nucleic acid useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
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Pred. No. 1.3e-58;
                                                                 Holcik M,
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                                                                   Baird S,
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             (UYOT-) UNIV OTTAWA.
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Best Local Similarity
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                                                                   Korneluk RG,
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                                                                                                   Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    himporage ages (AAT70836-41) respectively code for a new class of mammalian proteins (AAM19581-86) that are inhibitors of apoptosis (TAP). The murine xiap gene (for X-linked IAP gene) sequence was constructed from 12 overlapping clones isolated from a mouse embryo lambda-gtil cDNA library and from a mouse FIX II genomic library using human xiap cDNA as probe. IAP nucleic acids can be used to express IAP polypetides in cells and animals to inhibit apoptosis, and as primers and probes to identify and isolate additional IAP genes, as well as in methods for treating diseases
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                                                                                                                                                                                                        Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 198; DB 18;
100.0%; Pred. No. 1.3e-58;
1ve 0; Mismatches 0;
                Mackenzie AE;
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                                                                                                                                                                          Claim 11; Page 78-79; 219pp; English.
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Baird S, Tsang B;

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                                                                                                         Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA; degenerative disease; infectious disease; autoimmune disease; cancer; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated protein homologues of viral inhibitors of apoptosis - used modulate apoptosis for treatment of degenerative, infectious or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC
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                                     Mouse inhibitor of apoptosis protein homologue MIHA DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;
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212..1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMRA-) AMRAD OPERATIONS PTY LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09723501-A1
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                                                                                                                                                                                                                                                            Aus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaux DL;
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AAZ48862
ID AAZ48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the mouse XIAP protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibits compounds are used to treat proliferative diseases, specially cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharnyx, thyroid, central nervous system, prostate, colon, cetum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, cesistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of IAP or NAIP polypeptide - also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inducing apoptosis in proliferative mammalian cells with inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%; Score 194.8; DB 19; Length 2691; 99.0%; Pred. No. 1.9e-57; 7ative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mackenzie AE, Pratt C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korneluk R, Liston P,
672..2162
/*tag= a
/product= XIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Fig 4; 147pp; English.
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                                                                                                                                                                                                                                                                                           98WO-IB00781
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Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-467164/40.
P-PSDB; AAW69297.
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                                                                                                                                               W09835693-A2
                                                                                                                                                                                                                                                                                                                                                                  13-FEB-1997;
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Query Match

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Gaps

AAT72710;

RESULT 4
AAT72710
ID AAT7
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AC AAT7
XX
DT 16-S

1581 181 1641

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요

roprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; loid precursor protein; tissue-specific expression control; human APP; pathway modulator; gene therapy; gene; ds.

DNA of APP related human homologue hCP35211.

(first entry)

27-JUN-2002

AAK99405;

Neuroprotective; nootropic;

/product "Protein of human homologue hcp352111"

/note= "No start codon"

WO200226820-A2.

04-APR-2002

Location/Qualifiers

Homo sapiens,

ď 692..1528

/\*tag=

Konsolaki M;

Freuler F,

Finelli AL,

Zusman S;

Cohen D, Dengler UJ, Reinhardt MWHM, Zusma 2002-315796/35. P-PSDB; AAO20511

(NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

2000US-236893P

29-SEP-2000; 14-JUN-2001;

01-OCT-2001; 2001WO-EP11345

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This sequence encodes the human XIAP protein.

The invention relates to a method for screening a substance inhibiting the formation of a complex between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be of a complex between XIAP and TAB1 is detected. The substance can be used as a drug for axtracellular matrix protein production enhancement, cell induction, monocyte migration, physiologically active substance as ubstance and substance can be used growth inhibition, and beta-amyloid protein deposition. A weblace inhibiting the formation of a complex between TAB1 and XIAP as weblace as between TAB1 and TABP as the substance of the substa
                                                                                                                                                                                  Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TAK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosyppression; Transforming growth factor-beta; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening a substance which inhibits combination of the X-linked inhibitor of apoptosis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and/or type II receptor is useful as a drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 28-30; 43pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0130378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0130378
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                                                                                                                             Human XIAP coding sequence.
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUMOTO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-078337/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY59451
                                                                                                                                                                                                                                                                                                                                                                              Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                      JP11326328-A
                                                                 24 - MAR - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAY-1998;
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   AAZ48862;
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                                                                                                                        GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                  GGAGGGCICACGGAITGGAAGCCAAGTGAAGACCCCTGGGACCAGCAIGGJAAGTGCTAC 180
                        Gaps
                                 1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
                      ö
                    Indels
Score 173; DB 21;
Pred. No. 6.3e-50;
                  0; Mismatches
                                                                                                                                                              CCAGGGTGCAAATATCT 1070
                                                                                                                                                   CCAGGGTGCAAATACCT 197
              Matches 182; Conservative
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AAK99405 standard; DNA; 2404 BP.

RESULT 6
AAK99405
ID AAK9

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The invention relates to a transgenic fly whose genome comprises DNA encoding a polypeptide having the Abeta portion of human amyloid precursor protein (APP), fused to a signal sequence. The DNA sequence of a sequence at 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in the specification. The DNA sequence is operably linked to a tissue-conspecific expression control sequence. Expression of the sequence gives the fly an altered phenotype. The purpose of the invention is for function of genes or encoded polypeptides which modify the APP pathway The agent is a compound, triple helix DNA, antisense oligonucleotide, double stranded RNA molecule, ribozyme, or particularly an antibody. It is used to treat conditions such as Alzheimer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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Pred. No. 7.3e-50;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 111; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.4%;
Best Local Similarity 92.4%;
Matches 182; Conservative
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GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGGCGATAAAGTGAAGTGCTTCCA¢TGTGGA 120
                                                                     GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human X-linked inhibitor of apoptosis DNA.
                                                                                                                                                                                                                                                                                                                                                        AAA64901 standard; DNA; 2540
                                                                                                                                                                                                                                    1006 CCAGGGTGCAATATCT 1022
                                                                                                                                                                                                            181 CCAGGGTGCAAATACCT 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                 AAA64901;
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                                                                                                                                                                                                                                                                                                                                    AAA64901
                                                                                                                                                                                                                                                                                                              RESULT
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947 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2 genes (AAT70836-41) respectively code for a new class of mammalian proteins (AAM19581-86) that are inhibitors of apoptosis (IAAP). The xiap gene (for x-linked IAP gene) was isolated from a tag site that shows strong homology with the conserved ring zinc finger domain of baculovirus CpIAP and OpIAP genes. The gene was to express IAP polypeptides in cells and animals to inhibit apoptosis, and as primers and probes to identify and isolate additional IAP genes, as well as in methods for treating diseases and disorders involving apoptosis (anti-apoptotic gene therapy).
                                                                                                                                                                                                                                                                                                                                               Apoptosis inhibitor; x-linked inhibitor of apoptosis protein; XIAP; HIV, AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 173; DB 18; Length 2540;
Pred. No. 7.5e-50;
0; Mismatches 15; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liston P, Mackenzie AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 67-68; 219pp; English,
                                                                                                                                                                                                                                                                                                        Human apoptosis inhibitor xiap cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
34..1527
/*tag= a
                                                                                                                                                                                AAT70836 standard; cDNA; 2540 BP.
                                       96WO-IB01022.
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92.4%;
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95US-0511485.
                                                                                                                                                                                                                                                                     (first entry)
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P-PSDB; AAW19581.
                                                                                                                                                                                                                                                                                                                                                                                                                reperfusion in
diagnosis; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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04-AUG-1995;
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                                                                                                                                                                                                                       AAT70836;
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/\*tag= a /product= "X-linked inhibitor of apoptosis"

Location/Qualifiers 34..1527 /\*tag= a

BP

(first entry)

Ackermann EJ;

99US-0392580

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                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to antisense oligonucleotides designed to inhibit expression of the human X-linked inhibitor of apoptosis. The present sequence is the X-linked inhibitor of apoptosis DNA. Modified phosphorothioate 2'-methoxyethyl (2'-MGE) oligonucleotides mere effective inhibitors than unmodified oligonucleotides. The objective inhibitors than unmodified oligonucleotides are expression in cells and tissues in vitro. The oligonucleotides are also weekl for treating animals or humans, prone to a disease associated with X-linked inhibitor of apoptosis. The oligonucleotides may also be used prophylactically to prevent infection, inflammation or tumour
                                                                                                              Antisense compound useful for research reagents, diagnostics, prophylaxis and for treating disorders associated with X-linked inhibitor of apoptosis, modulates expression of X-linked inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Best Local Similarity 92.4%; Pred. No. 7.5e-50;
Matches 182; Conservative 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                Example 13; Column 43-48; 33pp; English.
WPI; 2000-498201/44.
P-PSDB; AAY99985.
                                                                                                                                                                                                                                 apoptosis
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15; Indels 0;

1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60

Best Local Similarity 92.4\*
Matches 182; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
                                                                                                                                                                            946 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
                                              885
                                                                              GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                               GGAGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease.
                                  TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young
                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding inhibitor of apoptosis, XIAP #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baird S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 135pp; English.
                                                                                                                                                                                                                                                                                                                           ABK93869 standard; cDNA; 2540 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AEGE-) AEGERA THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001; 2001WO-CA01379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000; 2000US-0672717.
                                                                                                                                                                                                                             CCAGGGTGCAAATATCT 1022
                                                                                                                                                                                                          CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-479562/51.
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P-PSDB; ABG65663
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                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-2002
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development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
                                                                                                                                                                                                                                                                                                                                                     946 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; laP; pancreatic cancer; embryontc development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection;
                                                                                                                                                                                    1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                     GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                                                                                                                                                                                                    GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis nucleic acid useful for treating cancer and other
                                                                                                                 Length 2540,
                                                                                                                                                    Indels
                                                                                  Seguence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding inhibitor of apoptosis, XIAP #2.
                                                                                                                87.4%; Score 173; DB 24; 92.4%; Pred. No. 7.5e-50;
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                                                                                                                                   ilarity 92.4%; Pred. No. 7.5e
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK93875 standard; cDNA; 3000 BP
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(AEGE-) AEGERA THERAPEUTICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antisense inhibitor of appenhancing apoptosis in a cell, proliferative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-2000; 2000US-0672717.
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                                                                                                                                                                                                                                                                                                                                                                                                                       1006 CCAGGGTGCAAATATCT 1022
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                                                                                                                                     Similarity
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                                                                                                                                                    Matches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK93875;
                                                                                                                   Query Match
                                                                                                                                     Best Local
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   regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treat, an applicative disease. The method is useful for treat, and isease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, panoreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP
                                                                                                                                                                                                                                             1482 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 1541
                                                                                                                                                                                                                                                                                                                                       GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                           GGAGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide; proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                               TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
apoptosis in a cell, comprising administering a negative
                                                                                                                                                                                                        ó
                                                                                                                                                                                   Length 3000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pratt C;
                                                                                                                                                                                                         Indels
                                                                                                                                                             Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;
                                                                                                                                                                                Score 173; DB 24;
Pred. No. 8e-50;
); Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
34..1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV55038 standard; cDNA; 5232 BP.
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/product= XIAP
                                                                                                                                                                                    87.4%;
92.4%;
                                                                                                                                                                                                                                                                                                                                                                                     CCAGGGTGCAAATATCT 1678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human XIAP coding sequence.
                                                                                                                                                                                                                                                                                                                                                                         CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1998 (first entry)
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baird S, Korneluk R,
Tsang B;
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                                                                                                                                                                                           Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW69294
                                                                                                                                        cDNA seguence
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                                                                                                                                                                                    Query Match
Best Local 9
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                                                                                                                                                                                                                            This sequence encodes the human XIAP protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specially cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharnyx, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents, High levels of the IAP or NAIP proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detected in many cancers and are associated with poor prognosis, resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NaIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome 2g12-g14; transforming growth factor beta receptor; TGFbetaR; c-Jun N-terminal kinase; JNK; gene therapy; osteoarthritis; cytostatic; cypothyrodidism; juvenila nephronophthisis; thrombophilia; cahcer; colorectal cancer; neonatal purpura filminans; autoimmune disease; diabetes; multiple sclerosis; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCAC#GTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Inducing apoptosis in proliferative mammalian cells with iphibitor of IAP or NAIP polypeptide – also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers thoolving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
847..1197
/*tag- a //rboduct- "Human inhibitor of apoptosis (IAP)-like protein-3 (HILP-3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGGAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. le-49;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IAP-like protein-3 (ILP-3) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВÞ
                                                                                                                                                                        Claim 13; Fig 1; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.48;
92.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1006 CCAGGGTGCAAATATCT 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retinal degeneration; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 182; Conserv
                                                                                                          p53 mutations
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The present sequence is human inhibitor of apoptosis (IAP)-like protein-3 (ILP-3) cDNA. The hILP-3 gene is located on chromosome 2q12-q14.

ILP-3 comprises a spacer region and a ring finger domain. The ILP interacts with transforming growth factor beta receptor (TGFbetaR) and modulates TGFbetaR activity. ILP-3 also moderately inhibits ILP-1 mediated c-Jun N-terminal kinase (JNK) activation when co-transfected with ILP-1. Such activity decreases or prevents apoptosis in a cell. ILP-3 is used in the area of genetic testing for predisposition to diseases, such as osteoarthritis, hypothyrodisis, juvenile nephronophthisis, thrombophilia, colorectal cancer and neonatal purpura fulminans owing to an ILP-3 deletion or mutation. The ILP is also used in the treatment of diseases associated with abnormal apoptosis such as cancer, autoimmune diseases, e.g., dlabetes and multiple sclerosis and neurodegenerative diseases including retinal degeneration. The ILP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene is also used in gene therapy for treating patients suffering from ILP-3 gene deletions or mutations.
                                                                                                                                                                                                                                                                              transforming growth factor beta receptor modulating activity, and the nucleic acids that encode them, useful for treating, e.g. diabetes and multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 TATGAAGCATGGATCATTACTTTTGGGATGTGGATATATTCAGTTAACAAGGAGCAGCTT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;
antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 157; DB 22;
Pred. No. 2.4e-44;
0; Mismatches 25;
                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 87-88; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK14677 standard; cDNA; 1758 BP
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Best Local Similarity 87.3%;
Matches 172; Conservative (
                                                      29-SEP-2000; 2000WO-US26735
                                                                                          99US-0157169
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                                                                                                                                                                                                       WPI; 2001-258135/26.
                                                                                                                                                                     Duckett C, Mir SS;
                                                                                                                                                                                                                              P-PSDB; AAE00359.
                                                                                          30-SEP-1999;
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                05-APR-2001
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ABK14677
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This invention relates to the nucleic acid and protein sequences of a novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences have homology to the IAP (Inhibitors of apoptosis) gene family which are thought to inhibit proteins by regulating the anti-apoptodic activity of the V-Rel and NF-kappaB family of transcription factors. The gene for IAPL7 is located on human chromosome 19. The nucleic acids of the invention are useful for screening to identify compounds that stimulate or inhibit the function or level of IAPL7, where the identified compounds are useful for treating hyper-proliferative diseases such as cancer. The protein sequences may also be used to lasease such as cancer. The protein sequences may also be used to landing techniques. Nucleic acids encoding IAPL7, may be used receptor binding techniques. Nucleic acids encoding IAPL7, may be used to solate full-length cDMAs and genomic clones encoding IAPL7. The nucleic acid amplification reaction and the primers and probes may also be used to isolate full-length cDMAs and genomic clones encoding IAPL7. The nucleic acid sequences are useful as diagnostic reagents for diagnosing a disease or a susceptibility to a disease by detecting mutations in the associated gene. The nucleic acid sequence is useful for producing transgenic animals. The IAPL7 protein sequence may also be used to generate an anti-IAPL7 antibody which is useful in earlied to generate an anti-IAPL7 antibody which is useful in vention of mRNA and protein in cells. The sequences of the invention are also useful as vaccines for inducing an immunological response in a mamman The present sequence represents the configuration and insure to the tensor of the human and manner the process of the invention and the present sequence represents the coding the human and manner to the tensor of the tensor of the human and manner to the tensor of the tensor of the human and the present encoding the human and the present encoding the human and the present encoding the human and the present en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 979 TATGAAGCCCGGCTCATTACTTTTGGGACATGGATGTACTCCGTTAACAAAGAGCAGGTT 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New inhibitor of apoptosis proteins and polynucleotides useful in vaccines for inducing an immune response against hyperproliferative diseases e.g. cancer
chromosome 19; vaccine; gene therapy; hyperproliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nammal. The present sequence represents the cDNA encoding inhibitor of apoptosis 7 (IAP7) protein of the invention
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                                                                                                                                                                                                                            /partial
/note= "No start codon shown"
                                                                                                                                                                                                protein"
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 33-35; 41pp; English
                                                                                                                                                                         /*tag= a
/product= "IAPL7
                            cancer; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2001; 2001WO-EP08287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERE ) MERCK PATENT GMBH.
                                                                                                                                               286..1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-188741/24.
P-PSDB; AAU75747.
                                                                                                                                                                                                                                                                                                 WO200210381-A1
                                                                               Homo sapiens.
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                                                                                                                             Key
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Gaps

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This invention relates to the nucleic acid and protein sequences of a novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences have homology to the IAP (Inhibitors of apoptosis) gene family which are thought to inhibit proteins by regulating the anti-apoptotic activity of the V-Rel and NF-KappaB family of transcription factors. The gene for IAPL7 is located on human chromosome 19. The nucleic acids of the invention are useful for screening to identify compounds that stimulate or inhibit the function or level of IAPL7, where the stimulate or inhibit the function or level of IAPL7, where the disentified compounds are useful for treating hyper-proliferative diseases such as cancer. The protein sequences may also be used to identify membrane bound or soluble receptors of IAPL7 by standard receptor binding techniques. Nucleic acids encoding IAPL7, may be used as hybridisation probes for cDNA and genomic DNA, or as primers for nucleic acid amplification reaction and the primers and probes may also be used to isolate full-length cDNAs and genomic clones encoding IAPL7. The nucleic acid sequences are useful as diagnostic reagents for the nucleic acid sequences are useful as diagnostic reagents for diagnosing a disease or a susceptibility to a disease by detecting
                     121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New inhibitor of apoptosis proteins and polynucleotides useful in vaccines for inducing an immune response against hyperproliferative
                                                                                                                                                                                                                                                                                                                                                         Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;
antiapoptotic; IAP; apoptosis; V-Rel; NF-kappaB; antibody;
chromosome 19; vaccine; gene therapy; hyperproliferative disease;
cancer; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="This sequence encodes amino acid
residues 1-133 of the protein shown in
AAU75747. No start codon shown"
                                                                                                                                                                                                                                                                                                                         Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "IAPL7 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 286..687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 36-38; 41pp; English.
                                                                                                                                                                                                              BP.
                                                                                                                                                                                                        ABK14679 standard; cDNA; 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2001; 2001WO-EP08287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000EP-0116452
                                                                                                 1159 CCAGGTTGCAAATATCT 1175
                                                                           181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases e.g. cancer
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mutations in the associated gene. The nucleic acid sequence is useful for chromosome localisation and tissue expression studies and is also useful for producing transgenic animals. The IAPL7 protein sequence may also be used to generate an anti-IAPL7 antibody which is useful in screening methods for detecting the effect of added compounds on the production of mRNA and protein in cells. The sequences of the invention are also useful as vaccines for inducing an immunological response in a mammal. The present sequence represents the human inhibitor of apoptosis 7 (IAPP7) cDNA #2 of the invention. This sequence is the same as the sequence shown in ABK14677 but has a stop codon at nucleotides 685-687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; inhibitor of apoptosis; IAP-like protein-2; ILP-2; chromosome 19413.9d.3, transforming growth factor beta receptor; TGFbetaR; c-Jun N-terminal kinase; JMK; gene therapy; glutarhacaciduria; cone rod retinal dystrophy-2; retinitis pigmentosa; colorectal cancer; T-cell acute lymphoblastic leukaemla; neurodegenerative disease; retinal degeneration; hyperferritinaemla cataract syndroms; autochmune disease; sinitiple sclerosis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                   1039 GCAAGAGCTGGATTTTATGCTATAGGTCAAGAGGATAAAAGTACAGTGCTTTCACTGGGGA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1099 GGAGGGCTAGCCAACTGGAAGCAAGAAGAAGATCCTTGGGAACAGCATGCTAAATGGTAT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a /product= "Human inhibitor of apoptosis (IAP)-like protein-2 (hILP-2)"
                                                                                                                                                                                                                                                                                                                               1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGGAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                        61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                                                                                                                                                                                  Score 149; DB 24; Length 1758
Pred. No. 1.5e-41;
0; Mismatches 30; Indels (
                                                                                                                                                                                                               Sequence 1758 BP; 489 A; 371 C; 470 G; 428 T; 0 other;
                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IAP-11ke protein-2 (ILP-2) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
2074..2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD03581 standard; cDNA; 4993 BP.
                                                                                                                                                                                                                                                    Query Match 75.3%;
Best Local Similarity 84.8%;
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-2000; 2000WO-US26735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1159 CCAGGTTGCAAATATCT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CCAGGGTGCAAATACCT 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-258135/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duckett C, Mir SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200123568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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P-PSDB; AAE00365

Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with transforming growth factor beta receptor modulating activity, and the nucleic acids that encode them, useful for treating, e.g. diabetes and multiple sclerosis

Claim 18; Page 94-98; 108pp; English.

The present sequence is human inhibitor of apoptosis (IAP)-11ke protein-2 (ILP-2) CDNA. The hilp-2 gene is located on chromosome 19413.4.

[11-2] CDNA. The hilp-2 gene is located on chromosome 19413.4.

[11-2] CDNA. The hilp-2 gene is located on chromosome 19413.4.

[11-2] CDNA. The hilp-2 gene is located on chromosome 19413.4.

[11-2] CDNA. The hilp-2 gene is located on a Carboxy-terminal ring finger domain. It interacts with transforming growth factor beta ceeptor (TGFbetaR) and modulates TGFbetaR activity. It also potently inhibits apoptosis induced by overaxpression of Bax or by Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNR) activity. ILP-2 such as cone-rod retinal dystrophy-2, retinitis plumentosa, colorectal cancer such as cone-rod retinal dystrophy-2, retinitis plumentosa, colorectal cancer and hyperferritinaemia-cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also used in the treatment of diseases associated with abnormal apoptosis such as cancer, autoimmune diseases associated diabetes and multiple sclerosis and neurodegenerative diseases including retinal degeneration. The ILP-2 gene is also used in gene therapy for retinal degeneration and ILP-2 gene is also used in gene therapy for treating patients suffering from ILP-2 gene deletions or mutations. 

Sequence 4993 BP; 1526 A; 973 C; 1196 G; 1297 T; 1 other;

Gaps ö Length 4993; 30; Indels Query Match
75.3%; Score 149; DB 22;
Best Local Similarity 84.8%; Pred. No. 2.3e-41;
Matches 167; Conservative 0; Mismatches 30;

ö 2083 TATGAAGCCGGGCTCATTACTTTTGGGACATGGATGTACTGGTTAACAAGAGGAGCTT 2142 1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60 ö g

ò Q

GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180 121 à g

181 CCAGGGTGCAAATACCT 197 ò

2263 CCAGGTTGCAATATCT 2279

Search completed: April 19, 2003, 01:52:57 Job time : 157 secs

Appli Appli Appli Appli Appli Appli Appli Appli

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Gaps
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                                                                                                                                                      Sequence Seq
                                                                                                                          Sequence
                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08511485

Patent No. 5919912
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mackeniate, Alexander E.
APPLICANT: Mackeniate, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2100
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COUNTRY: USA

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-NUG 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 617/542-5070
TELEFAX: 617/542-8906
                                       PCT-US96 12860-1

US-09-205-204-1

US-09-205-204-1

US-08-800-929A-7

US-08-509-13

PCT-US96-12860-13

PCT-US96-12860-13

US-08-800-929A-13

US-08-800-929A-13

US-08-800-929A-13

US-09-371-13

US-09-371-13

US-09-371-10
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100.0%; Score 198; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-61;
Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-283-144-2
US-08-448-722A-1
US-08-189-309B-1
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TELBEAX: 20154
INFORMATION POR SEQ ID NO; 9;
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
       US-08-511-485-9
   \begin{smallmatrix} 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.0&0.0&0.0&0\\ 0.
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STATE:
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                                                                                                                                                                                          April 19, 2003, 01:53:06; search time 43 Seconds (without alignments) 1412.140 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                    1 tatgaagcacggatcgttac.....acccagggtgcaaataccta 198
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Sequence 11,
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Sequence 7,
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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(Ggn2_6/ptodata/1/ina/5A_COMB.seq:*

(Ggn2_6/ptodata/1/ina/5B_COMB.seq:*

(Ggn2_6/ptodata/1/ina/6A_COMB.seq:*

(Ggn2_6/ptodata/1/ina/6B_COMB.seq:*

(Ggn2_6/ptodata/1/ina/RECTUS_COMB.seq:*

(Ggn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-511-485-9
US-09-212-971-9
US-09-617-053A-9
US-09-617-053A-9
US-09-511-485-3
US-09-392-580-1
US-09-392-580-1
US-09-800-923A-3
US-09-800-923A-3
US-09-332-319-3
US-09-332-319-3
US-09-332-319-3
US-09-312-97-9
US-09-128-155-16
US-09-128-155-16
US-09-128-155-16
US-09-128-155-16
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JS-08-511-485-7
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US-09-617-053A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441362 seqs, 153338381 residues
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                                                                                                                             nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                   US-09-654-743-51
198
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Match Length DB
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Sequence:
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147.4
147.4
134.4
109.6
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                                                                                                                                                                                              Run on:
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No.
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APPLICANT: Tails, Stephinal K
APPLICANT: Pratt, Christine
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
CORRESPONDENCE: 17 **
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1461 TATGAAGCACGGATCGTTACTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCTT 1520
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Pred. No. 1.9e-60;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
CLASSIFICATION 124
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 617-428-1046
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-0200
                        MacKenzie, Alexander
                                           Liston, Peter
Baird, Stephen
Tsang, Benjamin K
Pratt, Christine
                                                                                                                                                                                                                                                                                                                           E: Diskette
IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 2691 base pairs
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Matches 196; Conservative
                                                                                                                                                                                                                                                                                         ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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; MOLECULE TYPE:
US-08-800-929A-9
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APPLICANT: Korneluk, Robert G
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Pratt, Christine
APPLICANT: NOUP NOT BESSE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: 06/017,354
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER PLING DATE: 1996-11-14
EARLIER PLING DATE: 1996-11-14
EARLIER PLING DATE: 1996-11-14
EARLIER PLING DATE: 1997-02-13
NUMBER: OS SEQ ID NOS: 17
SOUTWARE: FastSEQ for Windows Version 4.0
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                                  916 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 975
                                                                                                      121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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Pred. No. 1.9e-60;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09212971B Patent No. 6107041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
                                                                                                                                                                                                1096 CCAGGGTGCAAATACCTA 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.4%;
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Best Local Similarity 99.0
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus
US-09-212-971-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q ID NO 9
LENGTH: 2691
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US-08-800-929A-9
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Sequence 9, Application US/09617053A Patent No. 6300492 GENERAL INFORMATION:

US-09-617-053A-9

RESULT 4

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GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAA¢TGCTAC 180
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US-08-511-485-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: U
                                                                                                                                                                                                                            RESULT 6
US-08-511-485-3
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APPLICANT: Morentuk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Tsang, Benjamin K
APPLICANT: Parat, Christine
TITLE OF INVENTION: DEFECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DEFECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
SOFTWARE: FASTESC for Windows Version 4.0
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98.4%; Score 194.8; DB 4; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.9e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0;
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Sequence 3, Application US/09239867
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.4%; Score 173; DB 4;
92.4%; Pred. No. 1.1e-52;
tive 0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1641 CCAGGGTGCAAATACCTA 1658
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                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3
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Best Local Similarity
Matches 182; Conserv
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US-09-239-867-3
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                                                                                                                                  Sequence 3, Application US/08511485
Patent No. 591912
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/511,485 FILING DATE: CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.4%; Score 173; DB 2;
92.4%; Pred. No. 1.3e-52;
tive 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUTICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8006
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
2540 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CCAGGGTGCAAATACCT 197
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Best Local Similarity 92.4'
Matches 182; Conservative
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EDNESS: both
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DETECTION AND MODULATION OF IAPS AND TREATMENT OF PROLIFERAT DISEASE
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                                                                                                                                                                                                                                                                                                                             1 TAIGAAGCACGGAICGTIACITIIGGAACAIGGAIAIACICAGIIAACAAGGAGCAGCII 60
                                                                                                                                                                                                                                                            Length 5232;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                      Query Match
87.4%; Score 173; DB 3;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 4.24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
                                                                                                                                       FEATURE:
NAME/KEY: variation
LOCATION: (4622)
OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3
                                                                                  NAME/KEY: variation
LOCATION: (4623)...(4623)
OTHER INFORMATION: n can be any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Faird, Stephen
APPLICANT: Fang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DEFECTION AND MO
TITLE OF INVENTION: IAPS AND NAIP FO
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08800929A Patent No. 6133437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1006 ccasssrarer 1022
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
2.1F: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtil
                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 17
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                                                                    FEATURE
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                                                                                                        Sequence 1, Application US/09392580
Patent No. 608713
Patent No. 608713
APPLICANT: C. Frank Bennett
APPLICANT: C. Flank Bennett
APPLICANT: C. Flank Bennett
APPLICANT: G. Prank Bennett
APPLICANT: G. Prank Bennett
APPLICANT: Lex M. COwsert
TITLE OF INVENTION: ANTIENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSIC CURRENT PEPLICANTION NUMBER: US/09/392,580
CURRENT PELLING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
LENGTH: 2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Normeluk, Robert G
APPLICANT: Hard.
APPLICANT: Liston, Peter
APPLICANT: Tang, Benjamin K
APPLICANT: Tang, Benjamin K
APPLICANT: Tang, Benjamin K
APPLICANT: Tang, Benjamin K
APPLICANT: Tang, Peter
APPLICANT: Pratt, Christine
ITILE OF INVENTION: DIFECTION AND MODULATION OF IAPS AND
ITILE OF INVENTION: DIFEASE
ITILE REPERBUE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARER: FASTSEQ for Windows Version 4.0
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Pred. No. 1.3e-52;
0; Mismatches 15; Indels
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Best Local Similarity 92.4%;
Matches 182; Conservative
1006 CCAGGGTGCAAATATCT 1022
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                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (34)..(1527)
US-09-392-580-1
                                                                                        US-09-392-580-1
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US-09-212-971-3
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US-09-121-979-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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0
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Pred. No. 1.9e-52;
0; Mismatches 15; Indels
                                                                                                                                                                                                                             ; LOCATION: 1...5232
OTHER INFORMATION: N at 4622 and 4633 can be A, G,
15-08-800-9294.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: (4623)
OTHER INFORMATION: n can be any nucleotide
LOCATION: (4622)
     07891/009001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUCATION: (4622)...(4622); OTHER INFORMATION: n can be any nucleotide US-09-617-053A-3
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Patent No. 6300492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEMCTH: 5.32 Dase pairs
TYPE: nucleic acid
STRANDEDNESS; single
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.4%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CCAGGGTGCAAATACCT 197
                                                TELEFAX: 617-428-7045
                                                                                                                                                         MOLECULE TYPE: CDNA FEATURE:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                          NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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US-09-617-053A-3
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LENGTH: 5232
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Gaps
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                                                                   1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGAGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTJGCTAC 180
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          Length 5232
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Pred. No. 1.2e-43;
0; Mismatches 31; Indels
       Score 173; DB 4; L
Pred. No. 1.9e-52;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09121979
Patent No. 6159709
GENERAL INFORMATION:
APPLICANT: KOTNELUK, Robert G.
APPLICANT: Liston, Peter:
TITLE OF INVENTION: XTAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021001
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INTENTION: XIAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021002
CURRENT APPLICATION NUMBER: US/09/332,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09332319
Patent No. 6171821
GENERAL INFORMATION:
   87.48;
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84.38;
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                                                                                                                                                                                                                                                                               181 CCAGGGTGCAAATACCT 197
Ouery Match
Best Local Similarity 92.4
Matches 182; Conservative
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Best Local Similarity 84.3
Matches 166; Conservative
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ORGANISM: Homo sapiens
US-09-121-979-3
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Sequence 16, Application US/09128155
Patent No. 611764
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILLE REPERENCE: 09404/05201
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER FILLING DATE: 1998-07-02
EARLIER FILLING DATE: 1998-07-02
EARLIER FILLING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/09128155
Fatent No. 6117654
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-07-02
EARLIER REPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1999-07-02
EARLIER FILING DATE: 1999-07-02
SARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,F,C or G
US-09-128-155-16
                                         181 CCAGGGTGCAAATACCT 197
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ORGANISM: Homo saptens
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LOCATION: (1)...(15233:
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US-09-128-155-16/c
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SEQ ID NO 17
LENGTH: 176373
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                                                                                                                                                                                                                                                                               1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                                                                                                    DB 4; Length 711;
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Patent No. 6331412

GENERAL INPORMATION:

APPLICANT: ROBERT G. KORNELUK et al.

TITLE OF INVENTION: MALE FERTILITY

FILE REFERENCE: 07691/018002

CURRENT FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 05/09/239,867

PRIOR APPLICATION NUMBER: 05/073,001

PRIOR FILING DATE: 1998-01-29

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                 31; Indels
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Pred. No. 1.8e-43;
0; Mismatches 31;
                                                                                                                                                                                               Score 147.4; DB 4.
Pred. No. 1.2e-43;
0; Mismatches 31.
CURRENT FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: 09/121.979
EARLIER FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
ENG ID NO 3
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; OTHER INFORMATION: n = A,T,C or G
US-09-239-867-1
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Best Local Similarity 84.3%;
Matches 166; Conservative
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Best Local Similarity 84.3%;
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CCAGGGTGCAAATACCT 197
                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-332-319-3
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ORGANISM: Homo sapiens
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Gaps

198

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database :

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Sequence 1, Appll Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 21, Appl Sequence 21, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 1065, Appl Sequence 1, Appl Sequence 243, Appl Sequence 3474, Appl Sequence 243, Appl Sequence 243, Appl Sequence 243, Appl Sequence 933, Appl Sequence 2560, Ap
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; Dedication No. US20020187946A1
; GENERAL INFORMATION:
APPLICANT: MacKenale, Alexander E.
APPLICANT: MacKenale, Alexander E.
APPLICANT: MacKenale, Alexander E.
APPLICANT: Daird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/00303
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER PEPLICATION NUMBER: PCT/1B96/01022
EARLIER FILING DATE: 1996-02-04
EARLIER FILING DATE: 1996-02-04
EARLIER FILING DATE: 1996-12-22
EARLIER FILING DATE: 1996-12-22
EARLIER FILING DATE: 1995-08-04
SARLIER FILING DATE: 1995-08-04
SARLIER FILING DATE: 1995-08-04
SARLIER FILING DATE: 1995-08-04
SARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FASTSEQ for Windows Version 3.0
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8 US-08-913-322-2

10 US-09-967-2

8 US-08-913-322-2

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10 US-09-778-927A-21

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9 US-09-778-927A-21

9 US-09-778-927A-21

9 US-09-778-927A-30

10 US-09-904-615-30

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10 US-09-755-686-1

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10 US-09-164-877-3474

US-10-176-528-1

US-09-822-246-3

US-09-854-883-243

US-09-854-883-243

US-09-684-883-243

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US-09-684-883-243

US-09-684-883-243

US-09-764-877-2950
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22.7 5504
22.7 6124
22.7 6133
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22.7 6228
22.7 6228
22.0 2291
15.8 2240
15.5 2790
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14.7 1010
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14.3 1503841
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13.9 2160
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13.7 69899
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CORGANISM: Mus musculus
US-09-201-936-9
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Sequence 5, Appli
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Sequence 11, Appl
Sequence 7, Appli
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Sequence 7, Appli
Sequence 13, Appl
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Sequence 1, Appli
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                                                                                                                                                                                                                                                 April 19, 2003, 02:27:21; Search time 66 Seconds (without alignments) 3013.686 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/DEC_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
                                    GenCore version 5.1.4_p5_4578 Copyright (c) 1993. - 2003 Compugen Ltd.
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US-09-964-899-38
US-09-961-899-38
US-09-974-592-3
US-09-974-592-3
US-09-971-17
US-09-954-591-16
US-09-954-591-16
US-09-974-592-5
US-09-974-592-5
US-09-974-592-5
US-09-974-592-5
US-09-974-592-11
US-09-974-592-11
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US-09-974-592-7
US-09-974-592-13
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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173 134.4 109.6 76

No.

Result

65.8 65.8 61.8 59.4

Gaps

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61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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APPLICANT: Korneluk, Robert G.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

TITLE OF INVENTION: 19904/003003

CURRENT FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/011,356

EARLIER FILING DATE: 1996-08-05

EARLIER FILING DATE: 1996-08-05

EARLIER PILING DATE: 1995-08-04

EARLIER PILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

EARLIER PILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 3

LENGTH: 2540

LENGTH: 2540
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87.4%; Score 173; DB 9;
Best Local Similarity 92.4%; Pred. No. 1.6e-50;
Matches 182; Conservative 0; Mismatches 15
                                                                                                                                                                                                   87.4%; Score 173; DB 9; 92.4%; Pred. No. 1.6e-50;
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OTHER INFORMATION: N may be any nucleotide
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/09201936; Publication No. US20020187946A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                  Matches 182; Conservative
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ORGANISM: Homo sapiens
                                                                                                              TYPE: DNA
CORGANISM: Homo Sapien
US-09-964-899~38
                                                                                                                                                                                                                             Similarity
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Best Local S
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    GGAGGCCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGAACCAGCATGCTAAGTGCTAC 180
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Patent No. US20020174446A1
GENERAL INFORMATION:
TITLE OF INVENTION: Identification of Genes involved in
TITLE OF INVENTION: Identification of Genes involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31612 A
CURRENT APPLICATION NUMBER: US/09/964,899
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR PLICATION NUMBER: 60/236,309
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Pred. No. 3.7e-58;
0; Mismatches 2; I
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US-09-974-592-9
'S Squence 9' Application US/09974592
'Patent No. US20020120121A1
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                                                                                                                   1096 CCAGGGTGCAAATACCTA 1113
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
                                                                                           181 CCAGGGTGCAAATACCTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGGTGCAAATACCTA 198
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Matches 196; Conservative
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LENGTH: 2691
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Sequence 17, Application US/10095407

Patent No. US20020164330A1

GENERAL INFORMATION:

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 09404/052001

CURRENT APPLICATION NUMBER: US 60/091,650

PRIOR APPLICATION NUMBER: US 60/091,650

PRIOR PILING DATE: 1997-08-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 17
           APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT PAPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR PPLING DATE: 1998-07-02
PRIOR PPLICATION NUMBER: US 60/091,650
PRIOR PPLICATION NUMBER: US 60/054,646
PRIOR PLILNG DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FRSESQ for Windows Version 3.0
SOFTWARE: FRSESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGGAGCTT 60
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Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 134.4; DB 9;
Pred. No. 3.6e-36;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LCCATION: (1)...(15231)
CTHER INFORMATION: n = A,T,C or G
US-10-095-407-16
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LCCATION: (1)...(176373)

CTHER INFORMATION: n = A,T,C or G

US-10-095-407-17
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86.4%;
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Best Local Similarity 83.2%;
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3119 CCANGGTGTAAATATCT 3103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND TITLE OF INVENTION: NATP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE FILLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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                                                                 121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n can be any nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 02 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/974,592 CURRENT FILING DATE: 2001-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-10-095-407-16/c
; Sequence 16, Application US/10095407
; Patent No. US20020164330A1
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09974592
Patent No. US20020120121A1
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MacKenzie, Alexander
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tang, Benjamin K
APPLICANT: Pratt, Christine
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Korneluk, Robert G
                                                                                                                                                                                1006 CCAGGGTGCAAATATCT 1022
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LOCATION: 4622
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Best Local Similarity
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Sequence 16, Application US/09954531

Sequence 16, Application US/09954531

Patent No. US2002016518041

GENERAL INFORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: US-05-07-07

CURRENT APPLICATION NUMBER: US/09/954,531

CURRENT FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-US-194-94-406-1055, Application US/09954456

Patent No. US20020115057A1

GENERAL INFORMATION:

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REFERENCE: 689-290-76

CURRENT APPLICATION NUMBER: US/09/954, 456

CURRENT APPLICATION NUMBER: US/60/233, 617

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: US/60/235, 637
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Pred. No. 2e-16;
0; Mismatches 50; Indels
                               1654 TCAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTT 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT 197
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SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.4%;
Best Local Similarity 67.9%;
Matches 106; Conservative
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US-09-954-456-1635
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                                                                                                                                                                                          12609 GGAGGGGGCTAACTGATTGGAAGCCCAGCGAAGACCCTTGGGAACAACAACATGATAAATGG 12668
                                                                                                       Db 12549 CTTTCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGT 12608
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                                                      58 CTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGT 117
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Pred. No. 1.9e-16;
0; Mismatches 50; Indels
19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mackenzie, Alexander G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baldo, Stephen
APPLICANT: Baldo, Stephen
APPLICANT: Baldo, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CURRENT APPLICATION NUMBER: 09/011,356
EARLIER PILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER PILING DATE: 1998-02-04
EARLIER RILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER PILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOUTWARE: FRASEE FRASEQ for WINGOWS VERSION 3.0
Mismatches
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OTHER INFORMATION: N may be any nucleotide
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; LOCATION: (2602)...(2602)
COTHER INFORMATION: N may be any nucleotide
US-09-201-936-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (2470)...(2470)
OTHER INFORMATION: N may be any nucleotide
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OTHER INFORMATION: N may be any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09201936
Publication No. US20020187946A1
                                                                                                                                                                                                                                                                                                      12669 CATCCAGGGTGTAAATATCT 12688
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Best Local Similarity 67.9%;
Matches 106; Conservative
  Conservative
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LENGTH: 2676
Matches 121;
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5030 AGTTAATCCTGAGCAGCTTGCAAGTGCGGGTTTTTATTATGTGGGGTAACAGTGAÅGATGT 5089
                                                                                                  102 GAAGTCCTTCCACTGTGGAGGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCCTGGGA 161
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INVOCACHION:
APPLICANT: KOTNELUK:
APPLICANT: MAGNEZICA, Alexander E.
APPLICANT: MAGNEZICA, Alexander E.
APPLICANT: Balrd, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMALIAN IAP DETECTION METHODS
TITLE OF INVENTION: MAMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07693/00303
CURRENT APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1995-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 195-08-04
NUMBER OF SEQ ID NOS: 195-08-04
SOFTWARE: FASTESQ for Windows Version 3.0
TVDE: NAD
                                                                                                                                                                                     162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/09201936
Publication No. US20020187946A1
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    RESULT 12
US-09-201-936-39
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APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/00904
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT APPLICATION NUMBER: US 09/617,053
PRIOR PELING DATE: 2000-07-14
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastsEQ for Windows Version 4.0
ELENGTH. 6669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 GAAGTGCTTCCACTGTGGAGGGGGTTCACGGATTGGAAGCCAAGTGAAGACCCTGGGA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGT 101
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                                                                                                                                                                                                                                                                                                                                                                                38.4%; Score 76; DB 10; Length 3076; 67.9%; Pred. No. 2e-16; Live 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6669;
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Best Local Similarity 67.9%; Pred. No. 2.8e-16;
Matches 106; Conservative, 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT 197
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PATENTIN VOWER: US/60/235,863
SOFTWARE: PATENTIN VORS: 2276
SEQ ID NØ 1635
LENGTH: 8076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (3677)...(3951); OTHER INFORMATION: n can be any nucleotide US-09-974-592-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09974592
Patent No. US20020120121A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexand
                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 67.9:
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-954-456-1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: MacKenzle, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin k
APPLICANT: Tsang, Benjamin k
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
TITLE OF INVENTION: NIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009004
                                                                                                                                                                                                                         102 GAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCC¶GGGA 161
                                                                                                                                                                                          42 AGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGT 101
                                                                                                                                                                  Gaps
                                                                                          Query Match
34.3%; Score 68; DB 9; Length 245.
Best Local Similarity 64.7%; Pred. No. 1.2e-13;
Matches 101; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     1085 GGAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTT 1120
                                                                                                                                                                                                                                                                                                                                                                                      162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT 197
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Patent No. US20020120121A1
GENERAL INFORMATION:
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-39
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42 AGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGT 101

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RESULT 15
US-09-880-107-3354
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                                                                                                                                                                                                                                                                                                              55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NALMELLE, ALEXANDER E, APPLICANT: MACHEL S, APPLICANT: MACHEL S, APPLICANT: MACHEL S, Stephen APPLICANT: Liston, Peter TILLE OF INVENTION: MAMALIAN IAP GENE FAMILY, PRIMERS, TILLE OF INVENTION: PROBES, AND DETECTION METHODS FILE REFERENCE: 07991/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT PILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER PELING DATE: 1995-12-22
EARLIER FILING DATE: 1995-09-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FLASLESQ for Windows Version: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 33.2%; Score 65.8; DB 9; Best Local Similarity 60.2%; Pred. No. 7e-13; Matches 109; Conservative 0; Mismatches 72;
                                                                                                                                                                                                                                                                                        1.2e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1226 GGAACATGCCAAGTTCCAAGGTGTGAGTACTT 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                        0; Mismatches
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 11
LENTH: 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (2412)...(2412)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7
                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  h 34.3%;
Similarity 64.7%;
01; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Korneluk, Robert G.
                                                                                                                                                                                      TYPE: DNA
ORGANISM! Mus musculus
US-09-974-592-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                             Query Match
Best Local Sim:
Matches 101;
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Gaps

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17 TTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGGAGCTTGCAAGAGCTGGATTTT 76

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                                            1124 ATTATGTGGGTCGCAATGATGTGTCAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTT 1183
                                                                                                                        77 AIGCITIAGGIGAAGGCGAIAAAGIGAAGIGCITCCACIGIGGAGGAGGAGGCICACGGAIT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2046 ATTATGTGGGTCGCAATGATGTCAAATGCTTTTGTTGTGGTGGCTTGAGGTGTT 2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AIGCITIAGGIGAAGGCGAIAAAGIGAAGIGCTICCACIGIGGAGGAGGGCICACGGATI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 GGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTACCCAGGGTGCAAA¶ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 TTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGAT†TT
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 4421-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALCHIN Ver. 2.1
ENGILL 3532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U37547
US-09-880-107-3354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3532;
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Pred. No. 8.1e-13;
0; Mismatches 72; Indels
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                                                                                                                                                                                                                                                                                                                                                    Sequence 3354, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.2%;
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Best Local Similarity 60.29
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo saplens
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

Run on:

April 19, 2003, 01:38:31 ; Search time 1057 Seconds (without alignments) 3033.781 Million cell updates/sec

US-09-654-743-51

198 1 tatgaagcacggatcgttac......acccagggtgcaaataccta 198 Scoring table: Sequence:

Title: 'Perfect scode:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

32308132 Total number of hits satisfying chosen parameters: 16154066 seqs, 8097743376 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

em\_estba:\* EST: \*

em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_esthum:\*
em\_estin:\*
em\_estin:\*
em\_estin:\*
em\_estip:\*
em\_estip:\*
em\_htc:\*
gb\_esti:\* em\_estfun: em\_estom:\* gb\_est3:\* gb\_est4:\* gb\_est5;\* gb\_est2: gb\_htc:\* 4:ss6\_de

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_mus:\* em\_gss\_other:\* em\_gss\_pro:\*

em\_gss\_mam:\*

em\_gss\_fun:

em\_gss\_rod:\*

AL573382 mn83e12.x BB663325 BB663325 BB650856 BB650856 BF659610 uz88e12.x BM220130 C0935E08-BQ552032 H4013A06-Description SUMMARIES BB663325 BB6650856 BF659610 BM220130 BQ552032 AI573382 П 628 9 617 10 504 10 318 12 566 13 584 14 Query Match Length DB 54.5 52.2 50.9 49.5 Score 168 108 103.4 100.8 98 Result ٠ اي

BM805359 AGENCOURT AU123207 AU123207 AV705807 AV706807 AW375598 QVO-CT017 AW375599 QVO-CT017 AW375599 QVO-CT017 AW375599 QVO-CT017 AW375599 QVO-CT017 AW376421 QVO-CT017	AW3.75649 QVO-CT017 AW846337 QVO-CT017 BE268377 601124994 AW375648 QVO-CT017 AW375625 QVO-CT017 BQ652590 AGENCOURT	B1961039 MONO1_5_C AQO11995 HS_2190_A BE847058 uw23a06.y BE851680 uw99b07.y AA197349 mu21c08.r	BJ045197 BJ045197 BM312708 1978a10.y. AA7021/7 4 2191908.s AV704923 AV704923 BI253303 602973538 BQ443248 AGENCOURT AA354707 EST63004 BM126304 1f04e09.y B9720079 AGENCOURT	B1/1/10 003058472 R83677 yp16f10 r1 B1326908 AR071EL01 AW375608 QV0-CT017 AW375611 QV0-CT017 BW494270 IPCGBr1_1 BR016190 uy32a08.y A1552965 vg63h10.y BF325539 CM0-AN000
6 10 AU70559 6 10 AV706807 1 10 AW75598 1 10 AW375598 2 10 AW875507 2 10 AW875507 2 10 AW846425 6 10 AW846425 6 10 AW846421	444444	91219	E	19 29 29 29 29 29 29 29 29 29 29 29 29 29
46.6 1177 45.6 536 42.5 7316 38.4 354 38.4 4502 38.4 532 38.4 532 38.4 532 38.4 532	4444400			
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7 8 6 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	c 17		0 0 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0 444444 0044444

## ALIGNMENTS

EST 16-APR-1999 us cDNA clone , mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (28)

Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Morewood, K., Steptoc, M., Thelsing, B., Allen, M., Bowers, Y., Person, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Schurk, R., Ritter Washurnk: Milson, R. and Wilson, R., The Mashurnk: McCann, R., The Mashurnk: McCann, R., McCann, R. Email: mouseesf@watson.wustl.edu
This clone is available royalty.free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand Contact: Marra M.Washu-NCI Mouse EST project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810 mn83e12.x1 Stratagene mouse Tcell 937311 Mus musculus IMAGE:550702 3' similar to TR:060989 060989 MIHA.; m AI573382.1 GI:4536756 Mus musculus house mouse. RESULT 1 A1573382/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION

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198 a
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LOCUS
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 617)

8 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,

Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda

V.M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki

D., Shibate, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,

Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

L Unpublished (2001)
                                                                                                                                                              /dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Corgan: blood, Vector: pBluescript SK-; Site_1:
BCORI: Site_2: Xhor; Cloned unddirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZaP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
137 clis g 211 t 2 others
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
AM., Konno,H., Okazaki,Y., Miramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                 Score 168; DB 9; Length 628;
Pred. No. 1.7e-43;
0; Mismatches 12; Indels
                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IndE: 550702"
/clone_lib="Stratagene mouse Tcell 937311"
//tissue_type="Tcell"
  ity sequence stop: 440. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.4%;
Matches 185; Conservative
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81-45-503-9216
High quality
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, H., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                              ., Sugahara
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prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wadi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please Visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 TGACACCTAAGGTGAAGGCGATAAAGTGAAGTGCTTTCACTGTGCAGGAGGGCTCACGGA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 TIGGAAGCCAAGIGAAGACCCCIGGGACCAGCAIGCIAAGIGCIACCCAGGGIGCAAATA 194
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Su
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/dev_stage="15 days embryo"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="D930039G22"
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Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases I to 504)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Kouda
(M., Koya, S., Matsuyama, T., Miyazaki, A., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H.,
Muramatsu, M., and Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. .10 (11), 1757-1771 (2000) Konno, H., Fukunishi Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penese. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
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BB650856 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230036005 5', mRNA sequence.
BB650856
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/clone="C230036005"
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDN Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University, Genome Sequencing Center

Clone distribution: NGI-GGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
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Mus musculus cDNA clone IMAGE:3676174 3'
060989 INHIBITOR OF APOPTOSIS PROTEIN 3;;
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7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R c 7 R 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 318)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue_type="spontaneous tumor, metastatic Stem cell oxigin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                          Score 103.4; DB 10; Length
Pred. No. 1.3e-22;
0; Mismatches 7; Indels
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Seq primer: -400p from Glbco
High quality sequence stop: 226.
Location/Qualifiers
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/clone="IMAGE:3676174"
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similar to SW:IAP3_MOUSE
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BF659610.1 GI:11924744
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Best Local Similarity 93.9%;
Matches 107; Conservative
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a 128 c
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Unpublished (1997)
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BF659610/c
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VERSION
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Length 318

DB 12;

Score 100.8;

50.98;

Gaps

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RESULT 5 BM220130/c DEFINITION

õ 셤 à g SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

ACCESSION VERSION KEYWORDS

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Contact: Yong Olan
Laboratory of Genetics
Mational Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Seasell Drive, Sulte 3000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: #4013 row: A column: 06
Seq primer: -21M13 Forward
High quality sequence stop: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584 bp mRNA linear EST 20-JUN-2002 H4013A06-3 NIA Mouse 7.4k cDNA Clone Set Mus musculus cpNA clone BQ552032
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 584)
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Assembly, verification, and initial annotation of NIA 7,4K mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pSPORT1; Site_1: Sall; Site_2: Not1; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
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                                                                                                                                                                                                                                                                                                                                               49.5%; Score 98; DB 14; Length 584; llarity 95.3%; Pred. No. 8.1e-21; Conservative 0; Mismatches 5; Indels
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/db_xref="niaEST:H4013A06-3"
/db_xref="taxon:10090"
/clone="H4013A06"
/clone=lib="NIA Mouse 7.4K cDNA Clone Set"
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                                                                                                                                                                     49.5%; Score 98; DB 13; Le 95.3%; Pred. No. 7.9e-21; 1ive 0; Mismatches 5;
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                            by Yulan Piao (NIA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Male genital ridge/mesonephros"
/dev_stage="12.5-dpc"
/lab_host="DH108"
/note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2:
Not1; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nla.nlh.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
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1 (bases 1 to
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Library (Long) Mus musculus cDNA clone C0935E08 3', mRNA sequence.
BM220130
                                                                                                                                     53 AGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCC 112
                                                                                                                                                                                                      317 AGCAGCTTGCAAGAGTTGGATTTTAAGCTTTAGGTGAAGGCGATAAAGTCAAGTGCTTTC 258
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Ridge/Mesonephros cDNA Library (Long)"
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Pred. No. 6.7e-22;
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/organism="Mus musculus"
/stran="C57BL/61"
/db_xref="niaE3T:00935E08-3"
/db_xref="taxon:10090"
                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0355 row: E column: 08
Seq Primer: -21M13 Forward
High quality sequence stop: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM220130.1 GI:17780130
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                            93.88;
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                                                                Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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                            Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteria; Primates; Catarrhini; Hominidae; Homo.
E 1 (Dases 1 to 716)
S Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Chen, Z., Chen, J., Gu, W., Y., Chen, J., Gu, Y., Gu, Y., Gao, X., Chen, Z., Gu, W. R., Chen, J., Chen, J., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA ADB clones
Lu Gnpublished (2000)
Contact: Zeguang Ham Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 536)

S Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K., Nagai,T., Sugano,S. and Isogai,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)

L Unpublished (2000)

Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 11-22-3966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV/U6807 ADB Homo sapiens CDNA clone ADBCOF01 5', mRNA sequence. AV706807
                                                                                                                                                                                                                                                                                                                              Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 GGTGAAGGTGATAAAGTAAAAGTGCTTTCACTGTGGAGGANGGCTAACTGATTGGAAGCCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 GGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pUC19FL3; mRNA from uninduced precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT
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This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 45.6%; Score 90.2; DB 9; 1 Similarity 86.7%; Pred. No. 2.6e-18; 98; Conservative 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib-"NT2RM1"
/cell_type-"teratocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo saplens"
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AUTHORS
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                                                                                          AUTHORS
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AV706807
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                                                                                                                                   ымвоэз59
AGENCOURT 6499731 NIH_MGC_124 Homo saplens cDNA clone IMAGE:5728685
57, mena sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  In Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nlh.gov
Tissue Procurement: Invitrogen
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
Plate: LLAM12724 row: m column: 06
High quality sequence stop: 409.
                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1177)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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    13;
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Pred. No. 9.8e-19;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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AU123207
AU123207.1 GI:10947923
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| BM805359.1 GI:19122182
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Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                            human.
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NT2 neuronal

Mon Apr 21 09:59:52 2003

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Pred. No. 7.7e-14;
0; Mismatches 50;
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/db_xref-"taxon:9606"
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High quality sequence stop: 354.
Location/Qualifiers
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Best Local Similarity 67.9%;
Matches 106; Conservative (
67.98;
                        Conservative
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      Best Local Similarity
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                        106;
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AW375594
                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW375598 341 bp mRNA linear EST 04-FEB-2000 QVO-CT0179-300999-024-f08 CT0179 Homo sapiens CDNA, mRNA sequence. AW375598.1 GI:6880161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001

Email: asimpsoneludwig.org.br
This asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV0&t2-QV0-CT0179-
300999-024-f08&t3-1999-09-30&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence start: 15
Location/Qualifiers
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 341)
                                                                                                                                                       /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                        85 GGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCA 144
                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            145 AGTGAAGACCCTGGGACCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                         Length 716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                216 AGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTAAGAACTACT
                                                                                                                                                                                                 5 others
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                         Score 84.2; DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                         Pred. No. 2.8e-16, 0; Mismatches 16
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/lab_host="SOLR"
                                                                                                                                                                                                 163 t

    .341
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="CT0179"

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Best Local Similarity
Matches 95; Conserv
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ORIGIN
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ACCESSION VERSION

à 셤 ö 윤 ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE JOURNAL COMMENT REFERENCE

FEATURES

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/dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
Fits sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-0V0&t2-0V0-CT0179-
300999-024-d06&t3-1999-09-30&t4-1)
Seq primer: puc 18 forward
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I (bases 1 to 354)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
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                                                                                                           80 AGITAATCCTGAGCAGCTTGCAAGTGCGGGTTTTTTATTATGTGGGTAACAGTGATGT 139
                                                                                                                                                                   102 GAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGGA 161
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Pred. No. 7.9e-14;
0; Mismatches 50; Indels
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247 TCAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV0-CT0179-240
300-175-h08&t3=2000-03-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence start: 6
High quality sequence stop: 401.
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                                                                                                                                                                   AW846507 402 bp mRNA linear EST 19-MAY-2000 QVO-CT0179-240300-175-h08 CT0179 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 402)
Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Garvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 CAAATGCTTTTGCTGTGGTGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT 246
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                        213 TCAACATGCCAAGTGGTTTCCAAGGTGTGAGTACTT 248
               162 CCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCT 197
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/note-"Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 776 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
AW375599 531 bp mRNA linear EST 04-FEB-2000 QV0-CT0179-300999-024-904 CT0179 Homo sapiens CDNA, mRNA sequence.
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mRNA sequence.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=QVO&t2-QVO-CT0179-300999-024-gO&&t3=1999-09-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 531.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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/db_xref="taxon:9606"
/clone_lib="CT0179"
/dev_grape="Adult"
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Laboratory of Cancer Genetics
                                                                                           AW375599.1 GI:6880162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Tolect. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=0V0-CT0179-070
300-143-d098513-2000-03-078.4-1)
Seq primer: puc 18 forward: 4
High quality sequence start: 4
High quality sequence stop: 531.

Location/qualiflers

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/db_xref="taxon.9606"
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/dev_stage="hadult"
/dev_stage="hadult"
/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; Anin-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196 716 Ludwig Institute for Cancer Research) profiles
Into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 532)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A. Bordin, S., Costa, F.F., Brustein, A., deolivaira, P. Matsukuma, A., Bala, G.S., Simpson, D. H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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QVO-CT0179-070300-143-a04 CT0179 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                    hotgun sequencing of the human transcriptome with ORF expressed
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Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196

from ORESTES PCR (U.S. Letters Patent application No. 196

into the pUC 18 vector. Reverse transcription of tissue many and coln amplification were performed under low
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 546)
Dias Neto,E.; Garcia, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva,W. Orr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
M.J., Soares,F.; Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-QV0-CT0179-070 Seq primer: puc 18 forward from High quality sequence start: 6 High quality sequence start: 6 High quality sequence stop: 546.
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11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

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Laboratory of Cancer Genetics
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sac
                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF sequence tags
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Team: OIPEBackFileIndexing Dossier: 09654743

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